REMARKS

Responsive to the requirement for restriction, Applicants hereby elect the polynucleotide claims 1-14, 17, 22, 23 and 27-29. Non-elected claims 15, 16, 18-21 and 24-26 have been cancelled without prejudice to, or disclaimer of, Applicants' rights to prosecute the subject matter thereof in an appropriate divisional application.

Insofar as election of a single sequence is required, Applicants hereby provisionally elect the sequence of SEQ ID NO:6, with traverse.

Insofar as the Office Action implies that the polypeptides of SEQ ID NOS: 4, 6, 8, 36 and 38 possess differences in function and have independent utilities which cannot be exchanged, it is in error, and reconsideration and withdrawal thereof are respectfully requested.

The five polypeptide sequences are all closely related have substantial common structure and function. SEQ ID NO:8 is the full length human PDGF-D sequence. SEQ ID NO:6 is a C-terminal fragment of SEQ ID NO:8 and is 100% identical to the 322 C-terminal amino acids of SEQ ID NO:8. SEQ ID NO:4 is an even smaller C-terminal fragment. Amino acids 14-200 of SEQ ID NO:4 are 96.8% identical to amino acids 184-370 of SEQ ID NO:8. SEQ ID NO:36 is the full length murine PDGF-D sequence. It is over 85% identical to SEQ ID NO:8. SEQ ID NO:38 is identical to SEQ ID NO:36 except for a six amino acid deletion at amino acids 42-47 of SEQ ID NO:36. All five of the sequences share an identical 21 amino acid stretch corresponding to amino acids 291-311 of SEQ ID NOS:8 and 36. With regard to claim 22, all five of the sequences incorporate the cysteine-rich characteristic sequence of SEQ ID NO:25, so that claim 22 reads on all five of the sequences. In addition, all five of the sequences share an identical stretch of 24 amino acids at the C-terminal end.

Moreover, the sequences can be exchanged for each other. The polynucleotides which encode each of these sequences hybridize with each other. Antibodies raised to the human PDGF-D polypeptides also recognize and bind to the murine polypeptides. Furthermore, the sequences all bind to the same

receptors: that is to say the human and the murine sequences both have been demonstrated to bind to the murine receptors (See Bergsten et al., Nature Cell Biology 3:512-516 (2001)).

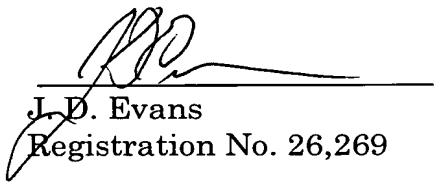
In view of the aforementioned common structural and functional characteristics, the polynucleotides encoding SEQ ID NOS 4, 6, 8, 36 and 38 form a proper Markush grouping pursuant to the provisions of MPEP §803.02 and are properly linked by, for example, claim 1, so that restriction among them is improper.

Favorable action on the application is earnestly solicited.

If there are any questions regarding this amendment or the application in general, a telephone call to the undersigned at (202) 624-2845 would be appreciated since this should expedite the prosecution of the application for all concerned.

If necessary to effect a timely response, this paper should be considered as a petition for an Extension of Time sufficient to effect a timely response, and please charge any deficiency in fees or credit any overpayments to Deposit Account No. 05-1323 (Docket #029065.44833C2).

Respectfully submitted,



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